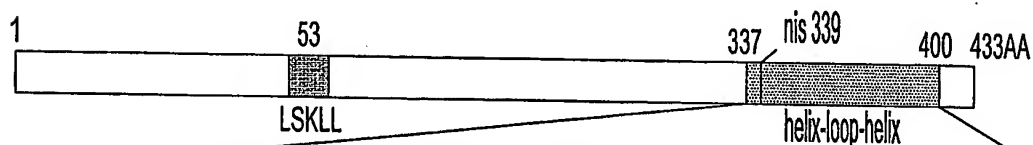
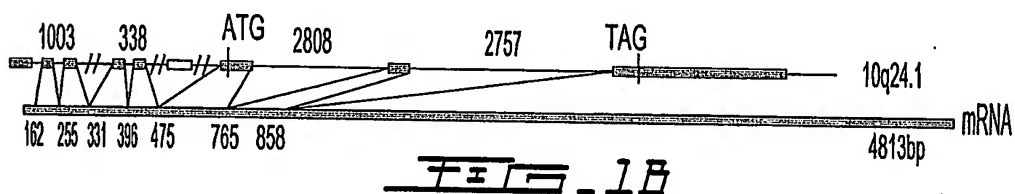
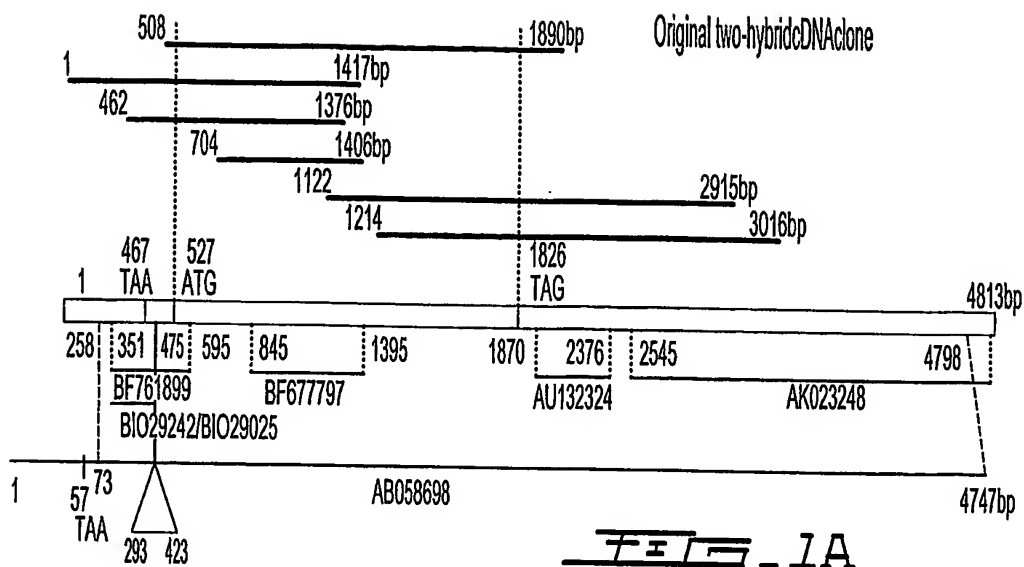
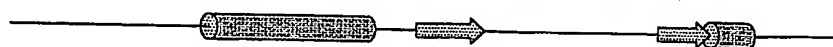


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LCoR	337	KOPRKKRGRVQYNSEILDEAISVMSGKMSVSKAOSTYGIPIHSTLEYKVKERLGLTKNP
EIP93F	741	KGTRPKRCKYVNYDRDSIVLAVKAVORCEMSVHRAGSYGVPHSTLEYKVKERHLMRPRK
T01C1.3	83	KRSRPKRGQYRKYDKNALDEAVRSVRRCMTVHRAGSFFGVPHSTLEYKVKERNLMRKKK
MBLK-1 repeat2	1041	KGTRPKRCKYVNYDRDSIVLAVRAVORCEMSVHRAGSYGVPHSTLEYKVKERHLMRPRK
MBLK-1 repeat1	579	VPVVGAGGGRAYTEELQALRDIQSCKLGTTRRAVLYGIPRSTLRNKVYKLAMERERD
PSQ repeat1	715	SGEKGGFNGPKAWTQDDMNSALDALKNQNMSTKASALYGIPTTLEWQRAHRMGIEPKK
PSQ repeat2	769	IETPKKEGTKSWNEDALQNALEALRSGQISANKASKAFGLPSTLEYKIARREGIRLAAP
PSQ repeat3	824	RLAAPFNAAPTTWTPTDIERALEAIRAGNTSVOKASAEFGIPTGTLEYGRCKREGIELSRS
PSQ repeat4	876	EGIELSKSNPTPWSEDAMNIALNSVRLQMSINQAAIHYNLPYSSLYGRFGRGKYDVVAN

* * * * *



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CCACGACAACCCACTGCAAGCAGATCCAGCAGCTGCTTCCTGTAATGCAGGACTCCCCAGGAGACCCAGGCATGGGCAGCAACCCCTGCA 91
 TGCCATTCTTTTGGGCTCCCGAGAACAGGGAGATAAACACCACCATCATCTGAGAGCCGGGAAGGGGAAGGCGAGGGTGTGTAGGCGGCAC 183
 GAATGCTCCGTTGAGAGACGCGGCTTTCGGCAAGAACTGGATTGCGGCCCCACAAGCTCATTCACTGTGTAGGTCCCGTTCCCTCTGTGC 275
 GGCGGCCGGGGACCATAAGGGCTTAACTCATATATTTAACCCCTCCAAAAAGGTTTGAAAGTATTCTTGAAGGGCTGTTGGACCTGC 367
 ATTATTAAGATCTCAGTTTATTAAAGACTGTGAACCTGAAAGCATTCTGATTGGACTTTTGATGAAAAGTGTATCTCTGTTGCTTGA 459
 GAAGAGATAAAGTAAAGACAGTCCCTGGGTCTCCGACCCCAATATTTCCCTAGTGGCCCGTGAGATC ATG CAG CGA ATG ATC CAA 544
 M Q R M I Q 6
 Q F A A E Y T S K N S S T Q D P S Q P N S T K 29
 CAA TTT GCT GCT GAA TAT ACC TCA AAA AAT AGC TCT ACT CAG GAC CCC AGC CAG CCC AAT AGC ACA AAG 613
 N Q S L P K A S P V T T S P T A A T T Q N P V 52
 AAC CAA AGC CTG CCG AAA GCA TCT CCA GTC ACC ACC TCT CCC ACG GCT GCA ACT ACT CAG AAC CCT GTG 682
 L S K L L M A D Q D S P L D L T V R K S Q S E 75
 CTC AGC AAA CTT CTC ATG GCT GAC CAA GAC TCA CCT CTG GAC CTT ACT GTC AGA AAG TCT CAG TCA GAA 751
 P S E Q D G V L D L S T K K S P C A G S T S L 98
 CCT AGC GAA CAA GAC GGT GTA CTT GAT CTG TCC ACT AAG AAA AGT CCA TGT GCT GGC AGC ACT TCC CTG 820
 S H S P G C S S T Q G N G R P G R P S Q Y R P 121
 AGC CAC TCT CCA GGC TGC TCC AGT ACT CAA GGG AAC GGG CGA CCT GGC AGA CCC AGC CAG TAC CGC CCA 889
 D G L R S G D G V P P R S L Q D G T R E G F G 144
 GAC GGA CTT CGG AGT GGT GAT GGG GTA CCT CCA AGA AGC TTA CAG GAT GGA ACC AGG GAA GGT TTT GGA 958
 H S T S L K V P L A R S L Q I S E E L L S R N 167
 CAC TCC ACA TCA CTC AAA GTT CCA CTG GCT CGA TCC CTG CAG ATT AGT GAA GAA CTA CTG AGC AGA AAC 1027

FIG. 11

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Q L S T A A S L G P S G L Q N H G Q H L I L S 190
 CAA TTG TCC ACA GCT GCC AGC CTT GGG CCA TCT GGA TTA CAG AAT CAT GGA CAA CAC TTA ATA TTA TCC 1096
 R E A S W A K P H Y E F N L S R M K F R G N G 213
 AGG GAA GCC TCT TGG GCA AAA CCA CAT TAC GAG TTC AAC CTC AGC CGT ATG AAG TTC AGG GGA AAT GGT 1165
 A L S N I S D L P F L A E N S A F P K M A L Q 236
 GCA CTC AGC AAC ATC AGT GAC CTT CCT TTT CTT GCA GAA AAC TCT GCC TTT CCA AAA ATG GCA CTT CAA 1234
 A K Q D G K K D V S H S S P V D L K I P Q V R 259
 GCA AAA CAA GAT GGA AAA AAG GAT GTG AGC CAT TCA TCT CCT GTA GAT TTA AAG ATA CCA CAA GTT CGA 1303
 G M D L S W E S R T G D Q Y S Y S S L V M G S 282
 GGA ATG GAT CTT TCT TGG GAG TCT CGC ACT GGT GAT CAG TAC AGC TAT AGC TCT TTG GTA ATG GGT TCA 1372
 Q T E S A L S K K L R A I L P K Q S R K S M L 305
 CAA ACG GAG AGC GCG CTT AGT AAA AAA TTA AGG GCT ATT CTT CCA AAA CAA AGT AGA AAA AGC ATG TTA 1441
 D A G P D S W G S D A E Q S T S G Q P Y P T S 328
 GAT GCT GGA CCC GAT TCT TGG GGC TCA GAT GCT GAG CAG TCT ACC TCT GGA CAG CCA TAT CCC ACA TCG 1510
 D Q E G D P G S K Q P R K K R G R Y R Q Y N S 351
 GAT CAA GAA GGA GAC CCT GGC TCC AAG CAG CCT CGG AAG AAA AGA GGG CGT TAC AGA CAG TAC AAC AGT 1579
 E I L E E A L S V V M S G R M S V S K A Q S I 374
 GAG ATA CTG GAG GAA GCA ATC TCA GTG GTT ATG AGT GGA AAA ATG AGT GTT TCC AAA GCT CAG AGT ATT 1648
 Y G I P R S T L E Y K V K E R L G T L R N P P 397
 TAT GGG ATT CCC CAC AGT ACA CTG GAG TAC AAA GTA AAG GAG AGG CTG GGC ACT TTG AAA AAC CCT CCA 1717
 K K K M K L M R S E G P D V S V K I E L D P Q 420
 AAG AAA AAG ATG AAA TTA ATG AGG TCG GAG GGG CCA GAT GTT TCT GTA AAG ATT GAA TTA GAT CCC CAG 1786
 G E A A Q S A N E S K N E * 433
 GGA GAG GCA GCA CAA AGT GCA AAT GAA TCA AAA AAC GAG TAG 1828

FIG. 11 (CONTINUE)

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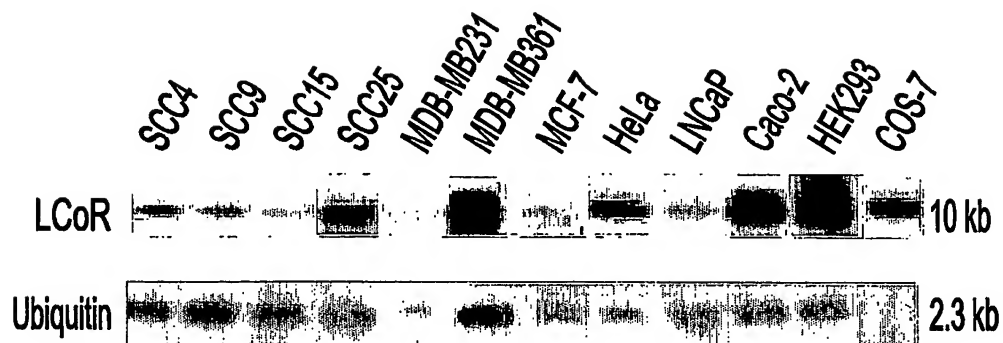
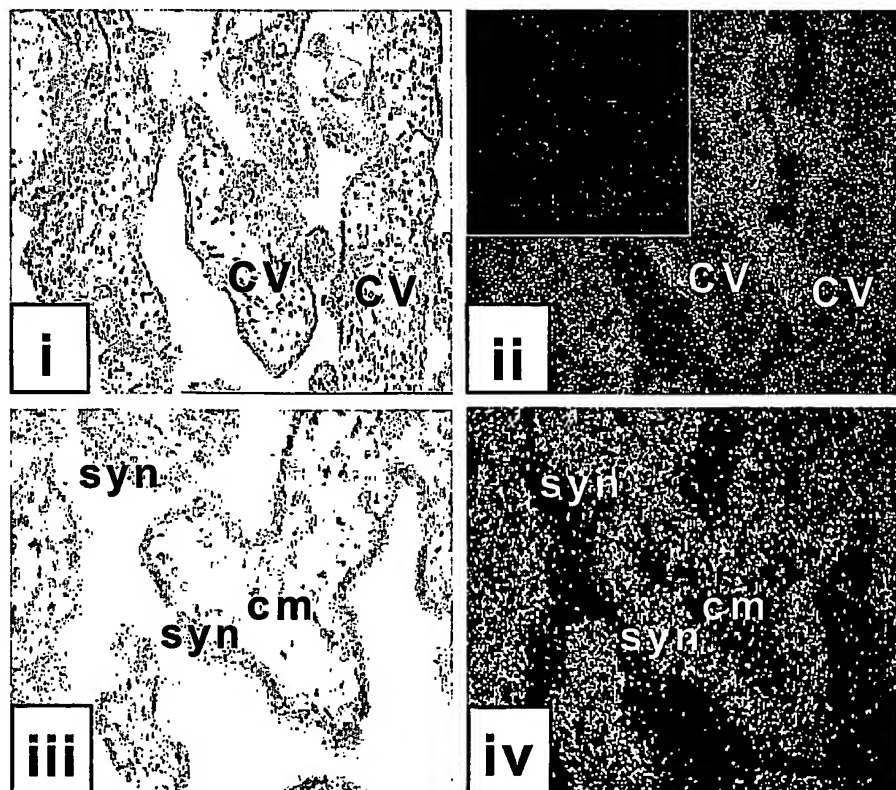
	1	2	3	4	5	6	7	8	9	10	11	12
A	whole brain	cerebellum, left	substantia nigra	heart	esophagus	colon, transverse	kidney	lung	liver	leukemia, HL-60	fetal brain	yeast total RNA
B	cerebral cortex	cerebellum, right	accumbens nucleus	aorta	stomach	colon, descending	skeletal muscle	placenta	pancreas	HeLa S3	fetal heart	yeast rRNA
C	frontal lobe	corpus callosum	thalamus	atrium, left	duodenum	rectum	spleen	bladder	adrenal gland	leukemia, K-562	fetal kidney	<i>E. coli</i> rRNA
D	parietal lobe	amygdala	pituitary gland	atrium, right	jejunum		thymus	uterus	thyroid gland	leukemia, MOLT-4	fetal liver	<i>E. coli</i> DNA
E	occipital lobe	caudate nucleus	spinal cord	ventricle, left	ileum		peripheral blood leukocyte	prostate	salivary gland	Burkitt's lymphoma, Raji	fetal spleen	Poly r(A)
F	temporal lobe	hippocampus		ventricle, right	ileocecum		lymph node	testis	mammary gland	Burkitt's lymphoma, Daudi	fetal thymus	human Col_1 DNA
G	p.g.* of cerebral cortex	medulla oblongata		inter-ventricular septum	appendix		bone marrow	ovary		colorectal adenocarcinoma, SW480	fetal lung	human DNA 100 ng
H	pons	putamen		apex of the heart	colon, ascending		trachea			lung carcinoma, A549		human DNA 500 ng

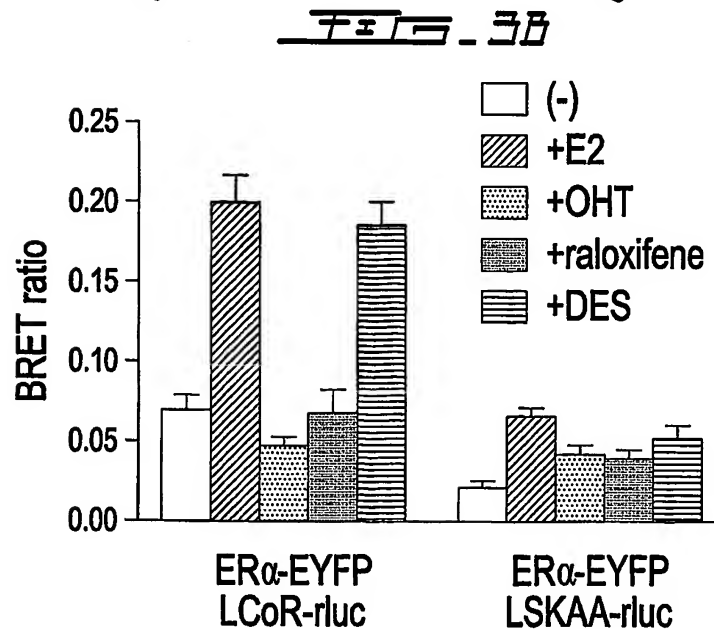
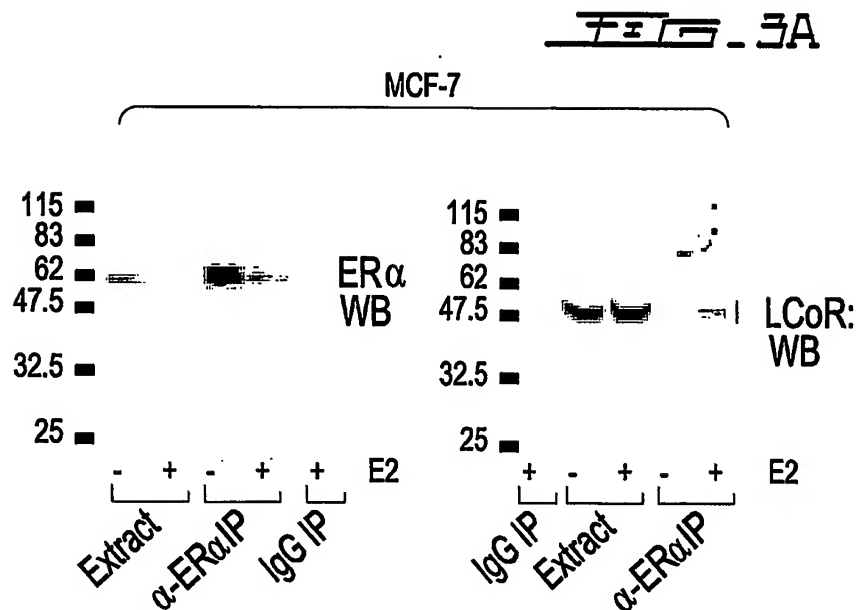
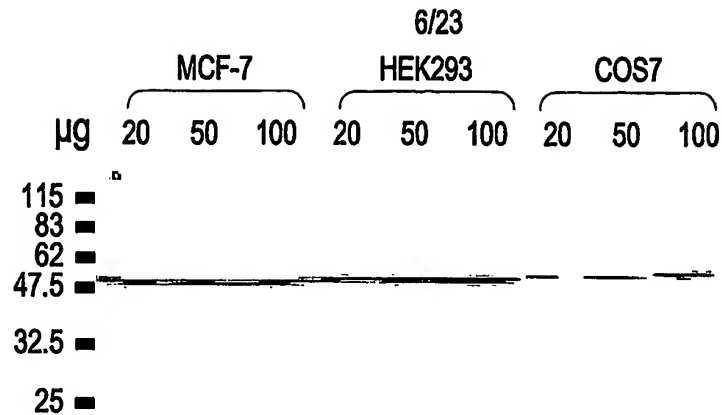
* paracentral gyrus

	1	2	3	4	5	6	7	8	9	10	11	12
A												
B												
C												
D												
E												
F												
G												
H												

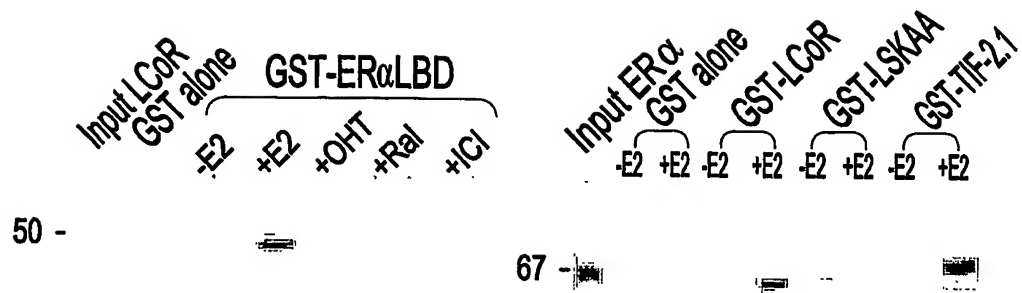
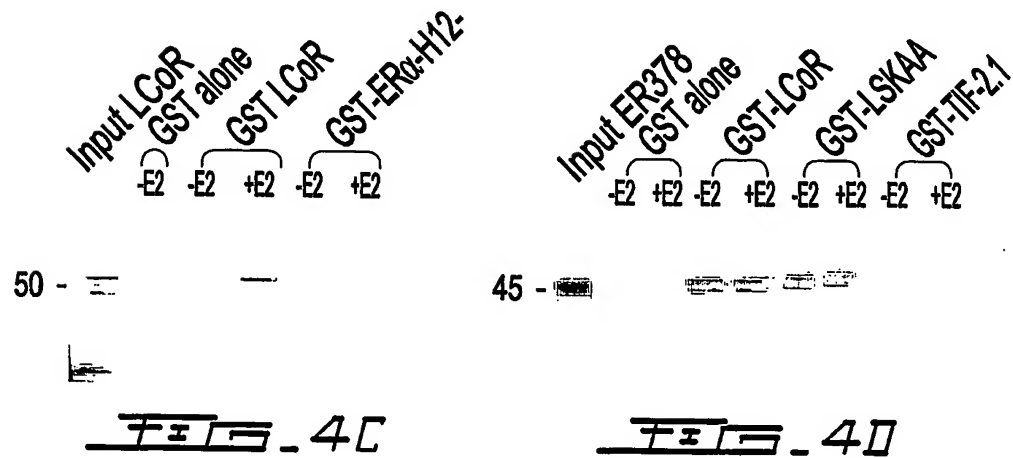
FIS-2A

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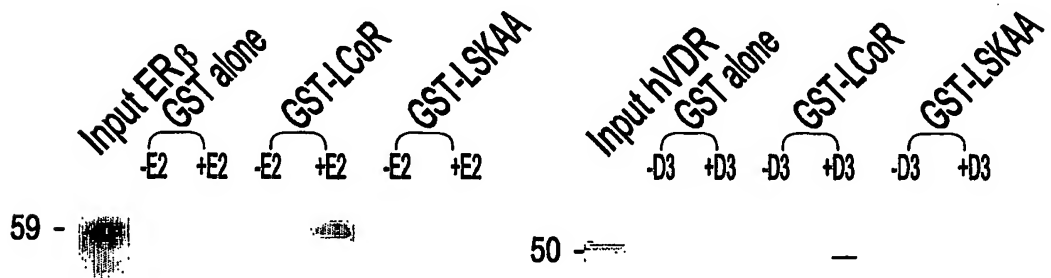
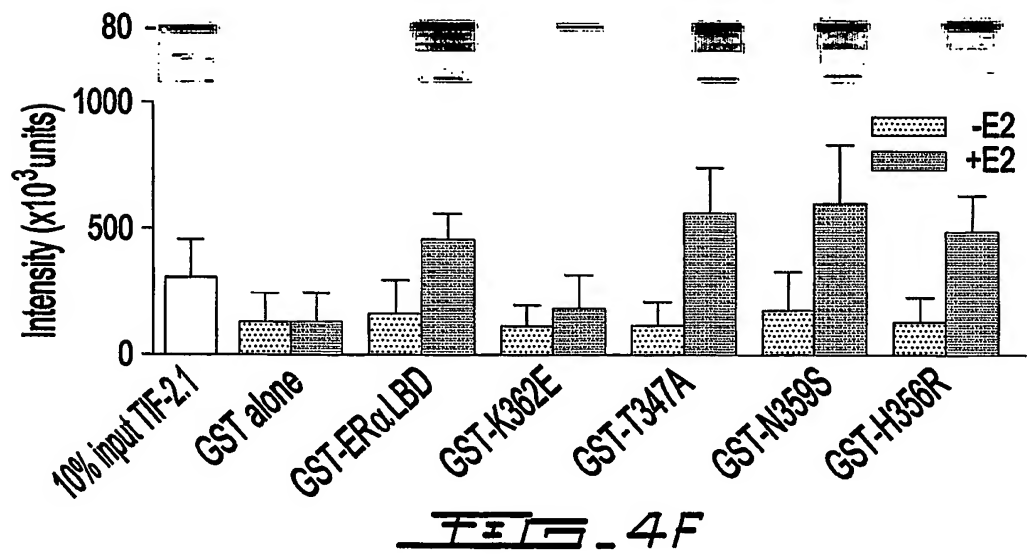
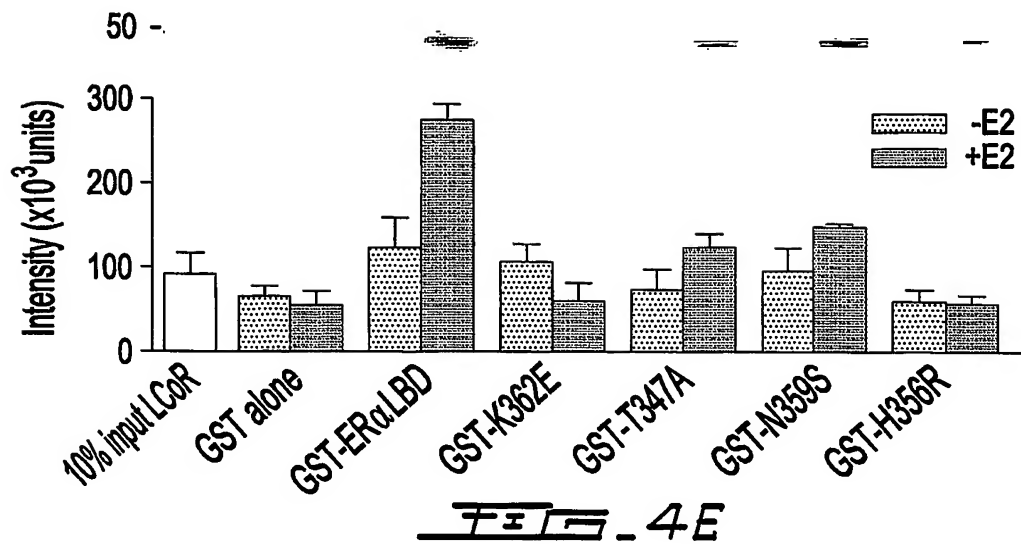
FIG. 2BFIG. 2C



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Fig. 4AFig. 4BFig. 4CFig. 4D

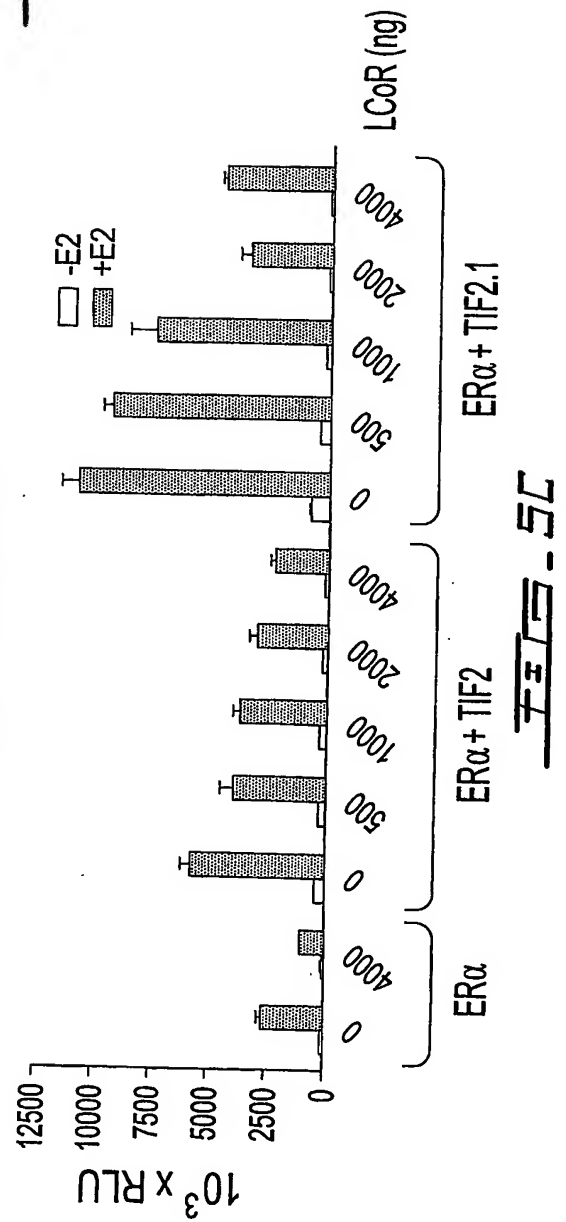
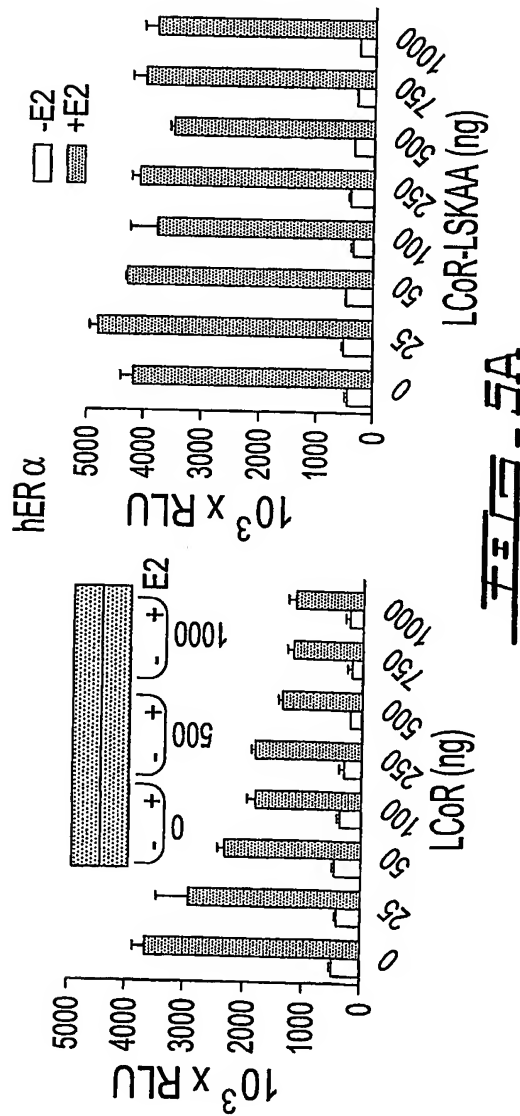
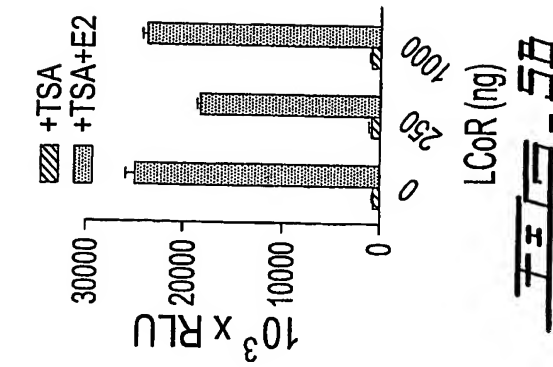
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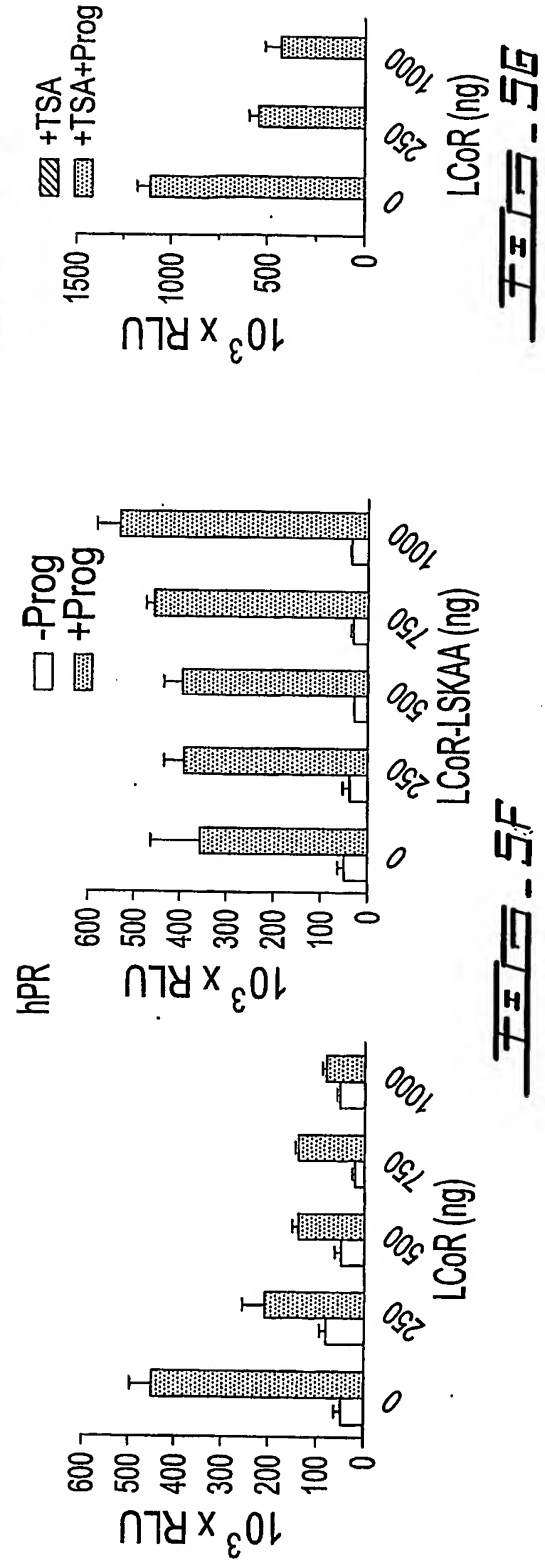
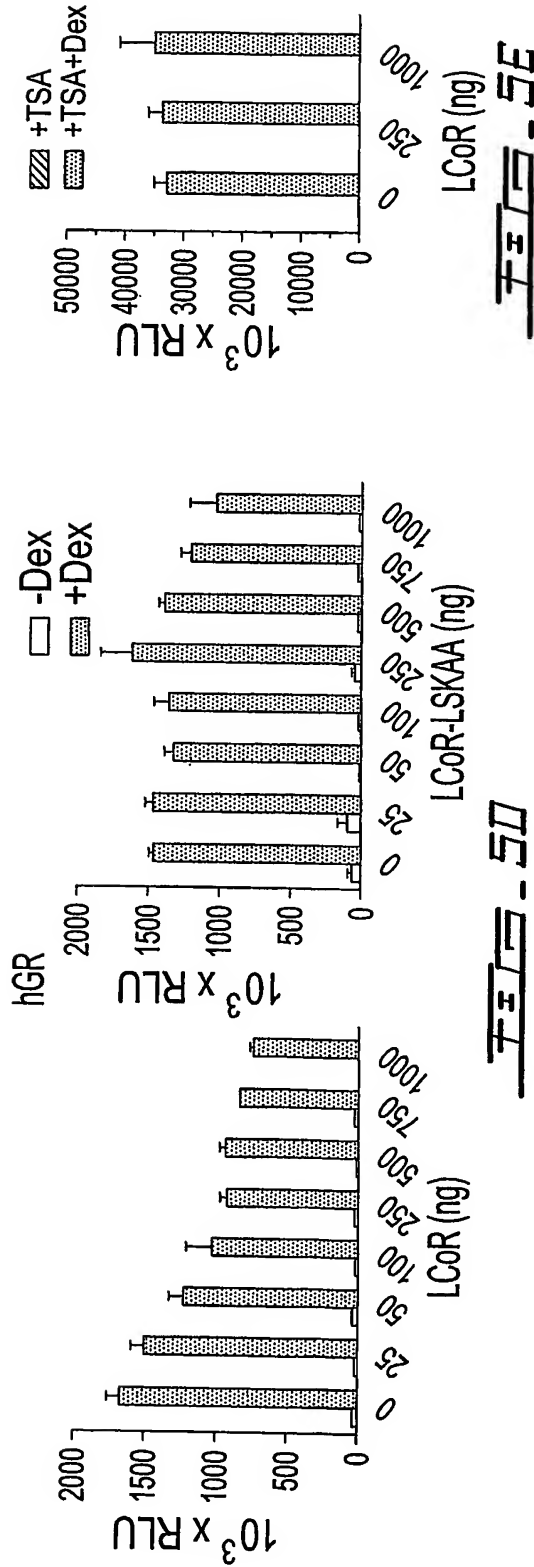
50

Fig. 4H

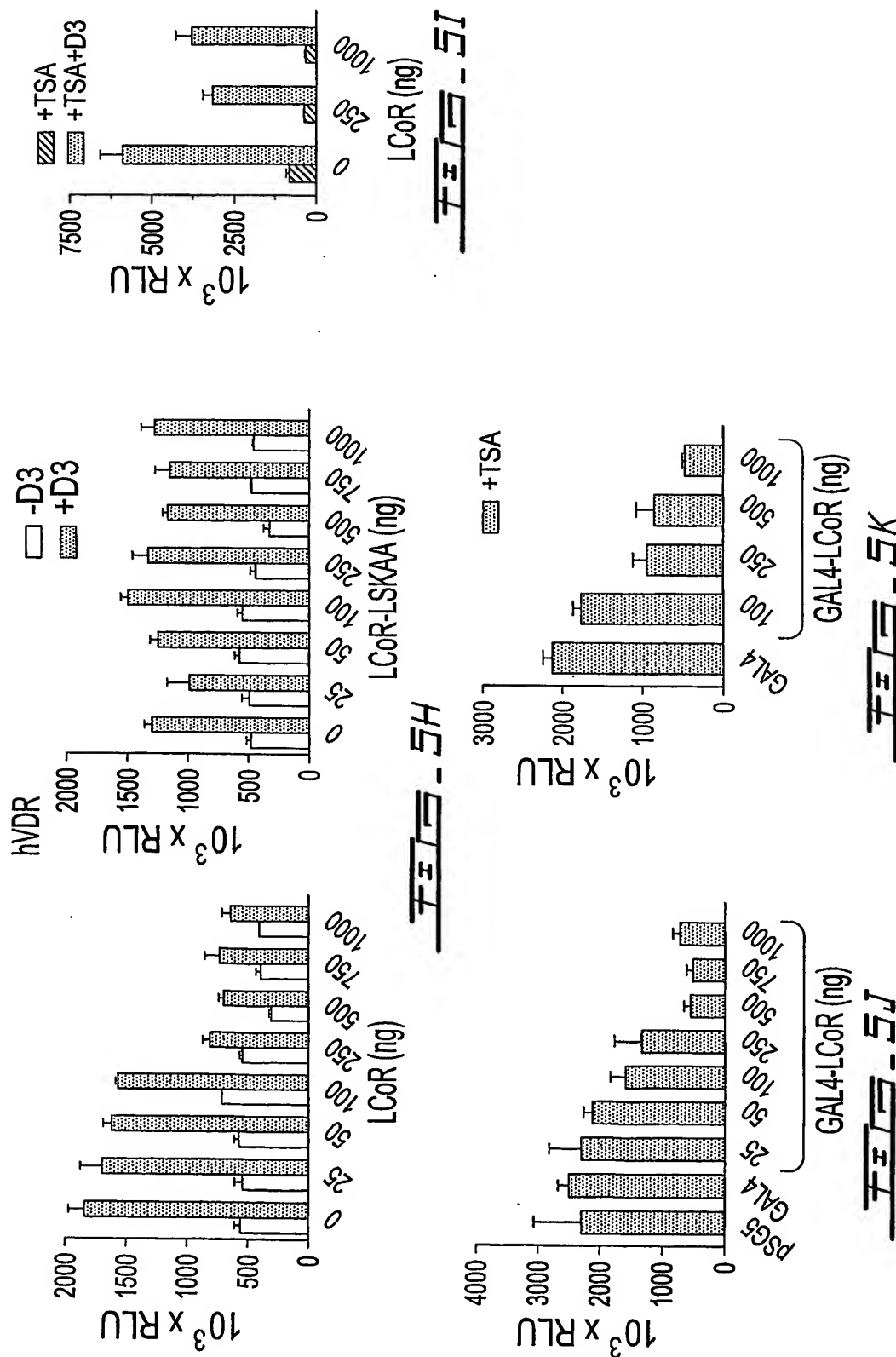
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Input HDAC3
GST alone
GST-LCOR
GST-LSKA4
Input HDAC6
GST alone
GST-LCOR
GST-LSKA4

- 146

- 49

Fig. 1A

Input HDAC1
GST alone
GST-LCOR
GST-LSKA4
Input HDAC4
GST alone
GST-LCOR
GST-LSKA4

- 125

- 55

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Extract				α -Flag IP				
+	-	-	+	+	-	-	+	F-LCoR
-	+	-	+	-	+	-	+	F-LSKAA
-	-	+	+	-	-	+	+	HA-HDAC3

49 -  HA-HDAC3
WB: α -HDAC3


50 -  F-LCoR
F-LSKAA
WB: α -Flag

FIG. 6B

MCF-7

WB: HDAC3

WB: LCoR

49 -  - 50

Extract
IgG IP
 α -HDAC3 IP

Extract
 α -HDAC3 IP
IgG IP

FIG. 6C

Extract				α -Flag IP				
+	-	-	+	+	-	-	+	HA-LCoR
-	+	-	+	-	+	-	+	HA-LSKAA
-	-	+	+	-	-	+	+	HA-F-HDAC6

146 -  HA-F-HDAC6

WB: α -Flag

 HA-F-HDAC6

50 -  HA-LCoR
HA-LSKAA
WB: α -HA

FIG. 6D

MCF-7

WB: HDAC6

WB: LCoR

146 -  - 50

Extract
 α -HDAC6 IP
IgG IP

Extract
 α -HDAC6 IP
IgG IP

FIG. 6E

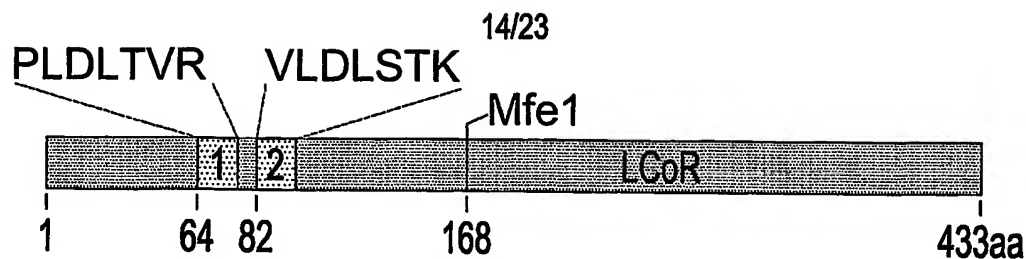
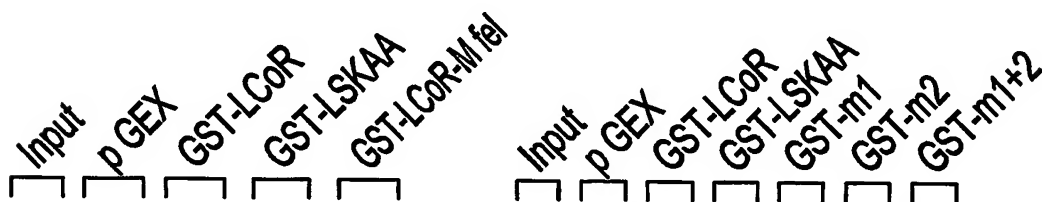


FIG. 7A



CtBP1

FIG. 7B

CtBP1

FIG. 7C

MCF-7

WB: LCoR

WB: CtBP1

WB: CtBP2



FIG. 7D

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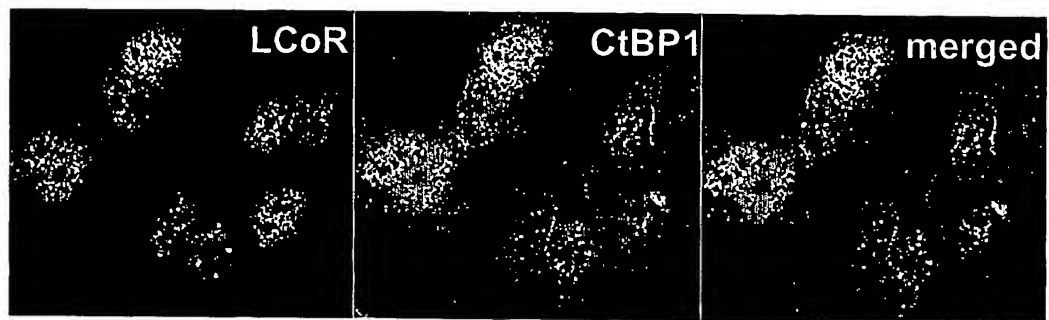


FIG. 7E

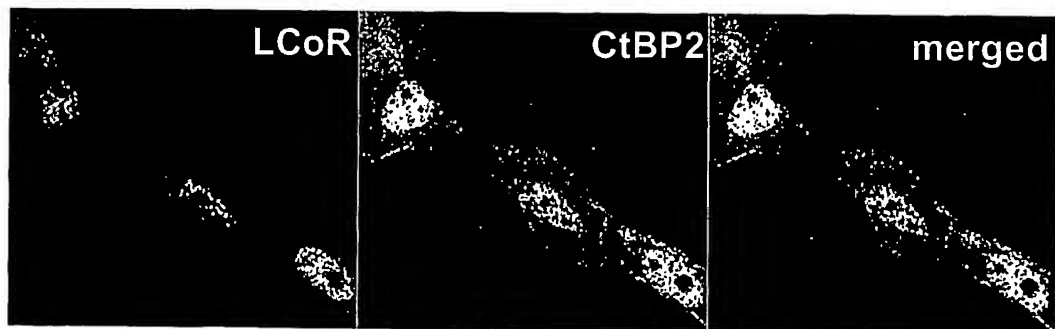


FIG. 7F

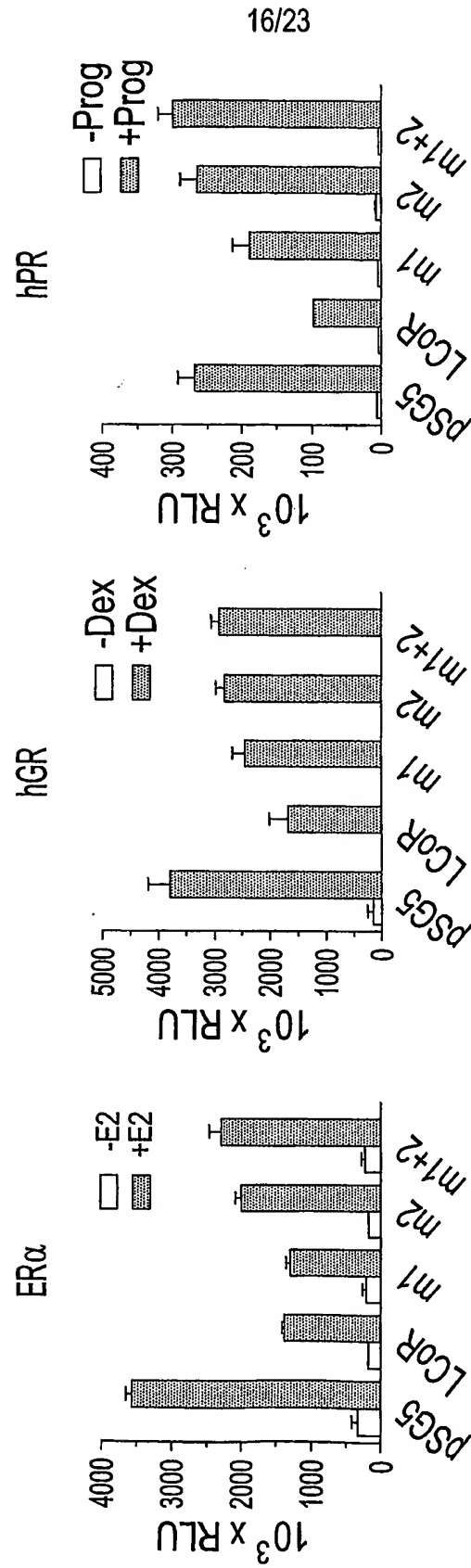
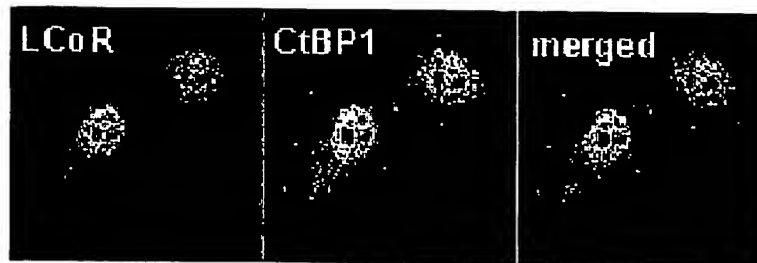
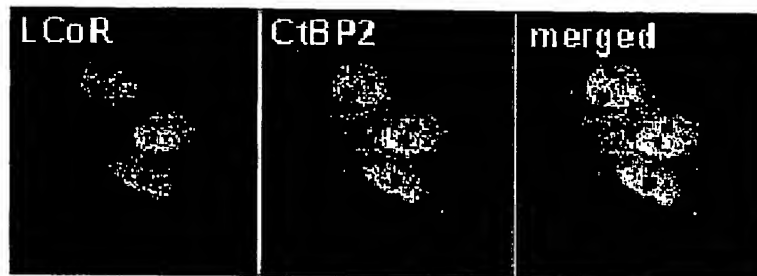
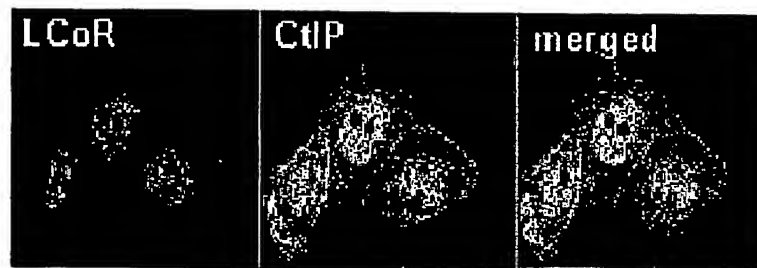
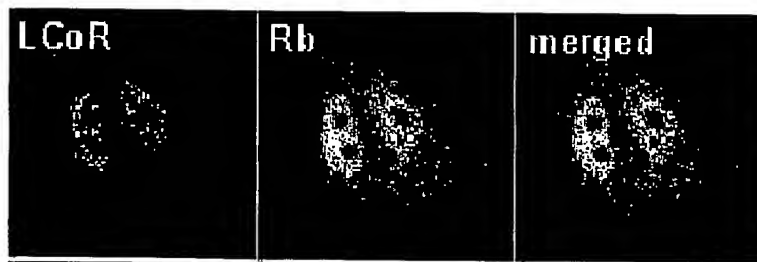
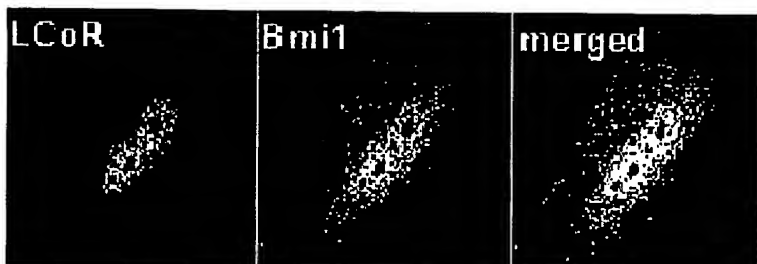


FIG. 7E

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FIG - 8AFIG - 8BFIG - 8CFIG - 8DFIG - 8E

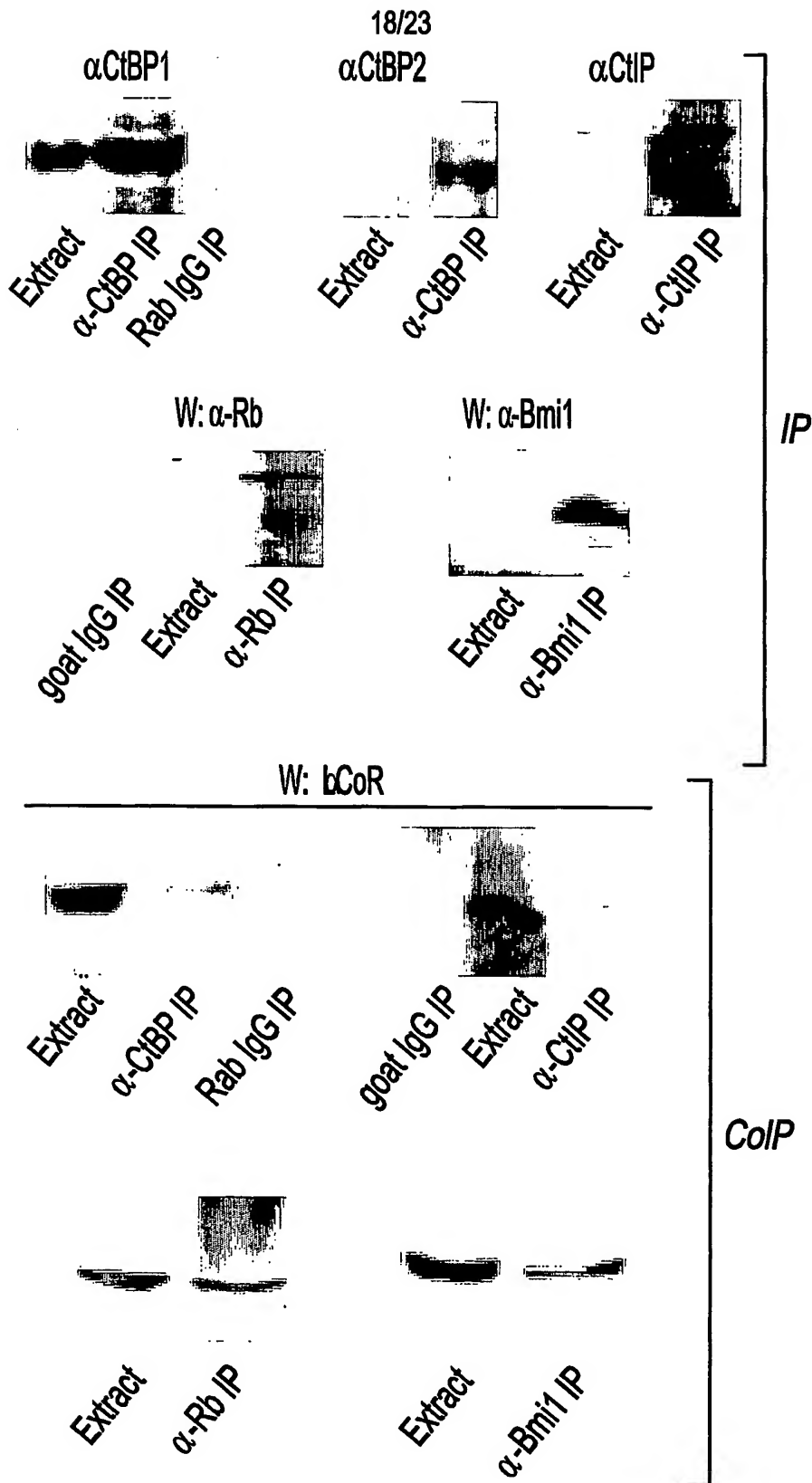
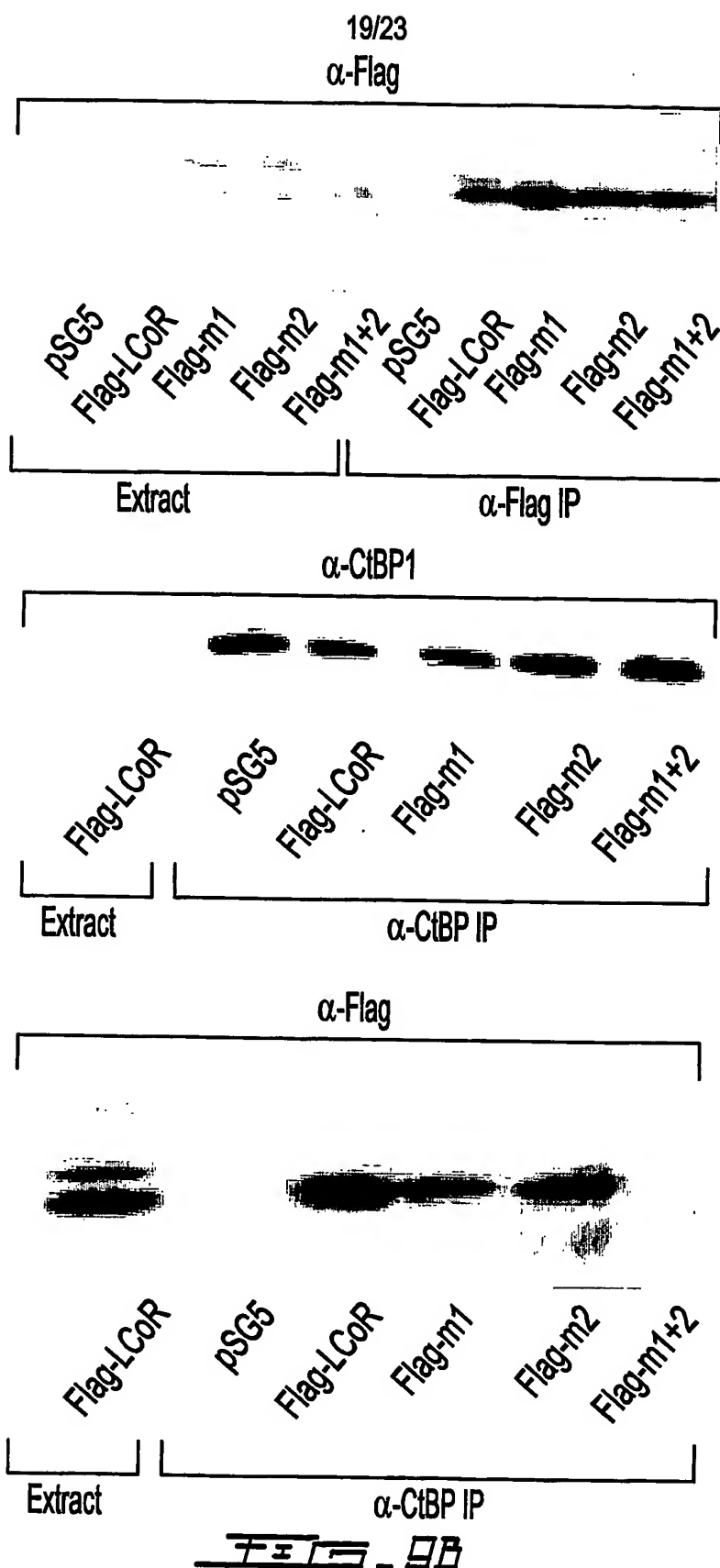
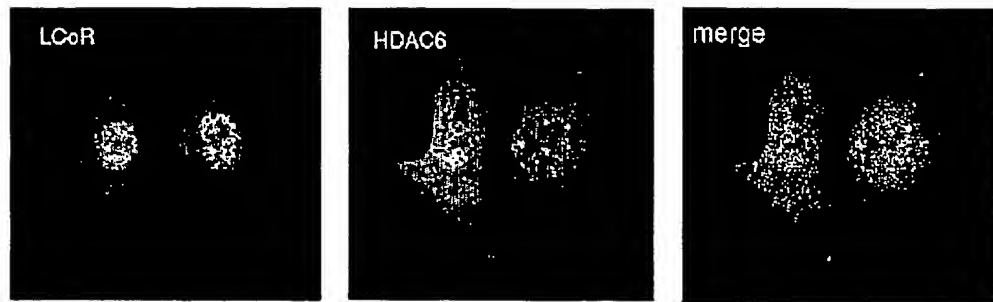


FIG. 9A



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FIG. 10AFIG. 10BFIG. 10C

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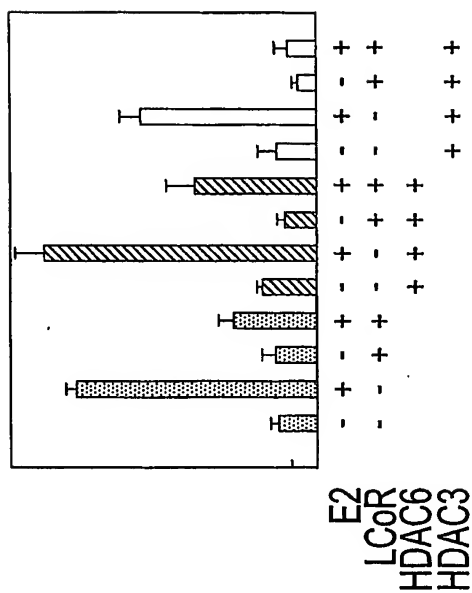


FIG - 100

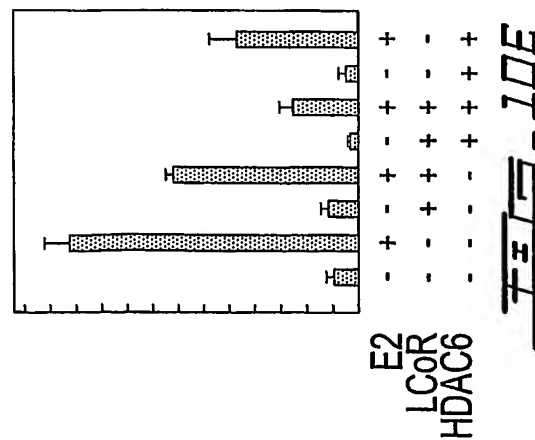


FIG - 10E

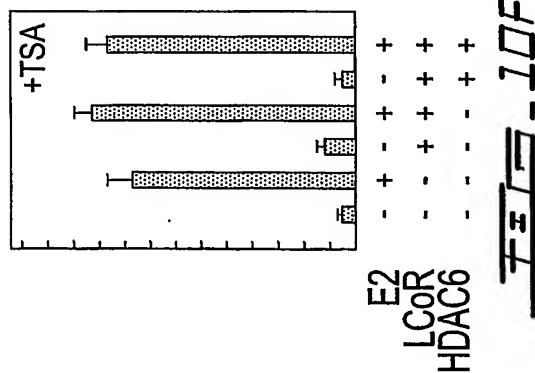


FIG - 10F

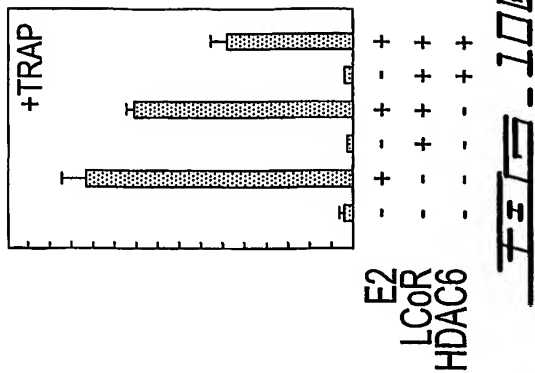


FIG - 10G

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FIG. 11AFIG. 11BFIG. 11C

